```
-Q-/cgn2_1/USFTC_spool/US09765034/runat_05122002_132016_21489/app_query.fasta_1.519
-DB=EST -OFMT=fastap -SUFFIX=P2n.rst -MINNATCH+0.1 -LOOPCL+0 -LOOPEXY=0
-UNITS-bits -START=1 -END-1 -MATRIX-biDsum62 -TRANS-human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALICH=15 -MODE=LOCAL
-OUTEMT-pco -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09765034_@CGN_1_1_763_@runat_05122002_132016_21489 -NCPU=6 -ICPU=3
-NO_XLPXY_NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMBOUT=120
-WARR_TIMEOUT=30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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-MODEL-frame+_p2n.model -DEV-xlh
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XGapop 10.0 , 1

YGapop 10.0 , 1

FGapop 6.0 , I

Delop 6.0 , I
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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ALIGNMENTS

AUTHORS TITLE	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BG402029	RESULT 1
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	1 (bases 1 to 877)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	EST.	BG402029.1 GI:13295477	BG402029	mRNA sequence.	602466748F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4594810 5',	BG402029 877 bp mRNA linear EST 12-MAR-2001		

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JOURNAL COMMENT
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Best Local Similarity:
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 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
                                                                                                                                                                                                                                                                    TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle
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                                                                                                                                                                                          AGGAGTTATGCCAATGGAAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLCM1336 row: p column: 11 High quality sequence stop: 542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: CLONTECH Laboratories, IncDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NIH_MGC_75"
/clone_lib="NIH_MGC_75"
/lab host="pH10B (Tl phage-resistant)"
/lab host="pH10B (Tl phage-resistant)"
/lab host="pH10B (Tl phage-resistant)"
/lab host="pH10B (Tl phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgttggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGACCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGACCGACGCGGCCGACTG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

98 a 221 c 199 g 259 t
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/db_xref="taxon:9606"
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VERSION
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                                                                                                                                                                  Query Match:
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Best Local Similarity:
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                                                                               AlaIleTrpVal-LeuValThrLeuGluLeuLeuProIleLeuProLeuIleAsnProVa 164
TAAGACTAACAGAGGCGCCACCCTTAATAATTTTACAAGGTGTGGAGACCCCAAAAACAA
                            lIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAs 184
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                                                               GCCATTTGGGTTTATAGTAACATTAGAGTTGCTACCCATACTTCACCTTAAGAATCCTGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 633)
Fujlyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes DNA, clu
AG083174
AG083174.1 GI:16634976
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing: M13Rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vector
                                                                                                                                                                                                                                                                                                                                                                    /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-080115.R"
/sex="male"
                                                                                                                                                                                                                                                                                                                      /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
129 c 149 g 158 t
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004B20 of
                           Submitted (12-APR-2000)
Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                 Unpublished 3 (bases 1
                                                                                                                                  2 (bases 1 to 1101)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                          Human gene number estimate provided Tetraodon nigroviridis DNA sequence
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1 (bases 1 to 1101)
Roest-Crollius,H., Jaillon,O., Dasi
Bernot,A., Fizames,C., Wincker,P.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provide
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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AL309576.1 GI:8216515
GSS; genome survey sequence.
Tetraodon nigroviridis.
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library A from Tetraodon
/organism="Tetraodon nigroviridis"
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                 rPheTyrIleValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTy
                                                ATCGCCTCTACGAAGGTTTGGACCGGAGTGGATCCATGCACGCTCGGGTACATCAAGGGG
                                                                        IleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThrGlnValValIle-AsnSe
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                       LysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPhe
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(bases 1 to 956)
(cost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, Cost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Cost-Crollius, J., Cost-Crollius, J., Cost-Crollius, C., Cost-Crollius
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 956)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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245P17 of
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a 214 c 290 g 176 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Tetraodon nigroviridis"
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lt,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                 (1-956)
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Mismatches:
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Gaps:
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                                                                                                                                           Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
E., Kohn,S., Shn,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI663305 520 bp mRNA uk27c10.yl Sugano mouse kidney mkia Mus IMAGE:1970226 5' similar to SW:P2YR_RAT
Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                     Unpublished (1999)
Other_ESTs: uk27cl0.xl
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P49651 P2Y PURINOCEPTOR 1
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US-09-765-034-2 (1-334) x AI663305
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                                                                                                                                ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64
                                                                                                                                                                                                                                                                                                          TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44
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AlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeu 158
                                                                            AACCTCTACACCAGCATGCTCTTGCTCACTGTCATTATCATGGACCGATATCTGCTCATG
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Seq primer
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer: custom primer used
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2 (bases 1 to 1026)
2 (crollius, H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
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Nat. Genet. 25 (2), 235-238 (2000)
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Exploration Research Group, RIKEN
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shitaki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tawaka,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanakka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-171 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sug
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/dev_stage="adult"
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/clone_lib="RIKEN full-length enriched,
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
usyashiraki
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Suc,Y. and Hayashizaki,Y.
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                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone="G430047C11"
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                                                                AUTHORS
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US-09-765-034-2 (1-334) x BB864882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 MetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACC 361
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                                                                                                                                                                                                            sequence.
BF196066
BF196066.1
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hr81f02.x1
1 (bases 1 to 589)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                             similar to
                                                                                                                                      Homo sapiens
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(cell_line=RCB-0646 Meth-A), (cell_line=RCB-0635 SUEHI-3),
(cell_line=RCB-0646 Meth-A), (cell_line=RCB-0545 OHTA),
(cell_line=RCB-0559 K-1 .F1), (cell_line=RCB-1283 B16
melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231
), (cell_type=Leydig cells, cell_line=CRL-2065 MLTC-1),
(cell_type=Nullipotent stem cell, cell_line=CRL-2070 NE),
(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=colon, cell_line=RCB-0549 Cle-H3), (tissue_type=colon, cell_line=RCB-0549 Cle-H3), (tissue_type=colon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), (strain=C3H, tissue_type=brain, cell_line=CRL-1443 BC3H1)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell_line=CCL-142 RAG), (tissue_type=submandibular gland, cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C, cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3B3
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                                                                                                                                                                                                                                                                                        589 bp mRNA linear EST 03-NOV-2000 NCI_CGAP_Kidl1 Homo sapiens cDNA clone IMAGE:3134907 3' SW:P2Y8_XENLA P79928 P2Y PURINOCEPTOR 8 ;, mRNA
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                                                                                Chordata; Primates;
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Catarrhini; Hominidae
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Query Match:
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                                                                                                                                                                                                                                         HisGluLeuLeuSerPheArgGluLys 334
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AW612141
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similar to
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
 Homo
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Location/Qualifiers
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                human.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
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/clone_lib="NCI_CGAP_Kid11"
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/db_xref="taxon:9606"
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                                                                                               639 bp mRNA linear EST 23-MAR-2000 NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2953309 3'SW:P2YR_CHICK P34996 P2Y PURINOCEPTOR 1; mRNA
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                                                       ACTGAGACACAACTTCAAATCCCTTACATCCTTTAGCAGATGGGCTCATGAACTCCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 449.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 639)
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National Cancer Institute, Cancer Genome Anatomy
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/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 582)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               info@image.llnl.gov
Seq primer: -40UP from Gibco
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CDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Fatima Bonaldo.
1 125 c 11
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/clone="IMAGE:3132688"
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,l, Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasal,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., T., Taraki, T., Sakai, K., Sano,H., T., Taraki, T
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                further details.
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Please visit our web site
                                                                                                                                                                             /clone="B430012021"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTAC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 MetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr 24
                                                                                                                                                                                                                                                                                                        GAAAGTGCCCTTTTTCGAAAAACACTTTTTTACAATAAGAAGGGAATTTGCGCCATTTATA 482
                                                                                                                                                                                                                                                                                                                                            eLysTyrProPheArgGlu~--HisLeuLeuGln~--LysLysGluPheAlaIleLeu--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGATAAGGGGACCTATGGAGATGTTCTTTGGATAAGCAACCGATATGGGCTTAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTCCATCTCTGACTTTGCTTTCCTGGGCACCCTTCCCATCCTGATAAAGAGTTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGTTTGGGTACCTGTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCTCTCTGGATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44
                                                                                                                                                                                                                            ATTTTCGCTTGGGGTGGCATGGGCCCTTTTA 513
                                                                                                                                                                                                                                                                                                                                                                                      AACCTTTAATCCAAGCTTACTTTACTTACTTATTTAGCATGGACCGATATTTGTTTAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                          AsnLeu-TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIl 124
                                                                                                                                                                                                                                                                -IleSerLeuAlaIle---TrpValLeuVal 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAla 104
                                                                                             BB846608 RIKEN full-length enriched, adult cDNA clone F530003124 5', mRNA sequence.
                                                                              cDNA clone
BB846608
Mus musculus
                                                           BB846608.1 GI:17084983
                     nouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCCCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified pBluescript KS(+) after bulk excision from Lambda
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426.00
72.85%
59.60%
24.38%
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Conservative:
Mismatches:
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VERSION

Pred.

Alignment Scores: Pred. No.:

5.47e-35 402.00

Length: Matches:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1650 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Wattahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
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Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayatsu, N., Hiramoto, K.,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Y. and Hayashizaki, Y.
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                           107
                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="F530003I24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="SOLR"
                        cleaved with XhoI and SstI.
c 87 g 129 t
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adult male kidney"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATGATAAGGGGACCTATGGAGATGTTCTATGTATAAGCAACCGATATGTGGTTCACAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAla 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTCATC-TCTGACTTTGCTTTCCTGTGCACCCTTCCATC-CTGATAAAGAGTTATGCC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus 6 days neonate head CDNA, RIKEN full-length enriched library, clone:5430432J15:purinergic receptor P2Y, G-protein coupled 2, full insert sequence.
                                Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yijiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikwa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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ency full-length cDNA
col. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Adachi, J., Alawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shibata, Y., Sakai, K., Sano, H., Sasaki, T., Sogabe, Y., Szuuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasaunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                                                                                                                                                                                                                                                                                                             BamHI. Host: DH10B.
                                                                     /strain="C57BL/6J"
/db_xref="FANTOM_DB:5430432J15"
/db_xref="MGD:MGI:1897121"
                                                                                                                                                                                   /organism="Mus musculus"
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/clone="5430432J15"
                                    /db_xref="taxon:10090"
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GCCCGAGAGCTCTTTAGCCATTTTGTGGCTTACAGCTCCGTCATGCTGGGTCTGCTTTTT
                                                                                    CGTTATGCCCGCCGGGTGGCTGCGGTTGTGTGGGTGCTGGTGCTGGCCAGGCACCC
                               SerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPhe 196
                                                                                                                                                              GluPheAlaIleLeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuPro 156
                                                                                                                                                                                                   AGCGTGCACCGGTGCCTGGGAGTCCTGCGCCCCTCTGCACTCCCTGCGTTGGGGCCCGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValLeuGlyAsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSer 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAATAGCACCATCAATGGCACCTGGGAGGGGGGACGAACTGGGATACAAGTGTCGTTTC
                                                                                                                                                                                                                              SerIleAspArgTyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLys 136
                                                                                                                                                                                                                                                                                                   SerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIle
                                                                                                                                                                                                                                                                                                                                  CTGTTGGTTTATTACTACGCCCGGGGTGACCACTGGCCATTTAGCACGGTGCTCTGCAAG
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/translation="MAADLEPPNSTINGTWEGDELGYKCRFNEDEKYVLLPVSYGVVC
/translation="MAADLEPPNSTINGTWEGDELGYKCRFNEDEKYVLLPVSYGVVC
/translation="MAADLEPPNSTINGTWEGLELGYKCRFNEDEKYVLLPVYYARGDHWPFS
TVLCKLVRFLEYTNLKCSILFILTGISYHRCLGYLRPLHSLRWGRARYARRVANVWVL
VLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVPFSVILVCY
VLMARRILKPAYGTTGGLPRAKRKSVBFIALVLAVFAKLGFLPFHLTRTLYYSFRSLDL
SCHTLNAINMAYKITRPLASANSCLDPVLYFLAGQRLVFFARDAKPPTEPTPSPQARR
KIGLHRPNRTVYKDLSYSSDDSRTESSTPAGSSTKDIKL"
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/dev_stage="6 days neonate"
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/db_xref="GI:12856589"
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Kawai,J., Shinagawa,A., Shidata,R., Indition, Adachi,J., Fukuda,S., Arakawa,T., Hara,A., Fukunishi,Y., Kondo,H., Adachi,J., Fukuda,S., Alzawa,K., Izawa,M., Nishi,K., Klyosawa,H., Kondo,S., Yamanaka,I., Aizawa,K., Izawa,M., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kanorta,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
                                                                                                                                                                                         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., RIKEN integrated sequence analysis (RISA) system-584-format sequencing pipaline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Larninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus adult male liver cDNA, R
library, clone:1300015C04:purinergic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (strain:C57BL/6J) adult clone_lib:RIKEN full-length enriched
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Rodentia;
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c receptor P2Y, G-protein
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mouse cDNA
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S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sofhrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamanura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cleaved with XhoI and SstI. Cloning sites, 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/)
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evidence: ISS
                                                                                                                                                                                                                                              /tissue_type="liver"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="FANTOM_DB:1300015C04"
/db_xref="MGD:MGI:1895057"
                              /gene="P2ry2"
/note="data source:MGD,
                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain-"C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                       /dev_
                                                                                                                                                                                                                                                                                                                                                                         /clone="1300015C04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="taxon:10090"
                                                                                                                                                                                                               _stage="adult"
                                      source key:MGI:105107
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 TrpAsnAlaThrCysLys---AsnTrpLeuAlaAlaGluAlaAlaLeuGlu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValLeuGlyAsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSer 57
LeuIleProLeuPheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGln
                                                                                                                                GTGCTCTACTTCGTCACCACCAGCGTGCGGGGGAACCCGGATCACTTGCCATGACACCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetLeuIleArgSerTyrAlaAsnGly---AsnTrpIleTyrGlyAspValLeuCysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAATAGCACCATCAATGGCACCTGGGAGGGGGGACGAACTGGGATACAAGTGTCGTTTC
                                               GCCCGAGAGCTCTTTAGCCATTTTGTGGCTTACAGCTCCGTCATGCTGGGTCTGCTTTTT
                                                                                   SerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPhe 196
                                                                                                                                                                        IleLeuProLeuIleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAla
                                                                                                                                                                                                                   GluPheAlaIleLeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuPro 156
                                                                                                                                                                                                                                                                                                      AGCGTGCACCGGTGCCTGGGAGTCCTGCGCCCTCTGCACTCCCTGCGTTGGGGCCGGGCC
                                                                                                                                                                                                                                                                                                                                              SerIleAspArgTyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLys 136
                                                                                                                                                                                                                                                                                                                                                                                           CTGGTGCGTTTCCTCTACACCAACCTCTACTGCAGCATCCTCTTCCTCACCTGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                 SerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIle 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGTTGGTTTATTACTACGCCCGGGGTGACCACTGGCCATTTAGCACGGTGCTCTGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuPro
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/db_xref="GI:12836639"
/db_xref="MGI:105107"
/db_xref="MGI:05107"
/translation="MAADLEPWNSTINGTWEGDELGYKCRENEDFKYYLLPVSYGVVC
VLGCCLNVVALYIELCRLKTWAASTTYMFHLAVSDSLYAASLPLLVYYYARGDHWPFS
TVLCKLVRELFYTNLYCSILFLTCISVHRCLGVLRPLHSLRWGRARYARRVAAVVWVL
VLACQAPVLYEVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLPAVPFSVILVCY
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                                                                                            1278 TACTACTCCGATCA------CTTGACCTCAGCTGCCACACCCTCAACGCCATC 1328
                                                                                                                                                                                            1158 CCGGCTTATGGGACCACAGGAGGTCTGCGCTCAGGCCCAAGCGCAAGTCTGTGCGCACCATT 1217
                                                                                                                                                              255 ArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCys---ThrGlnValValIle 273
                                                                                                                                                                                                                                                             217 ArgAsnArgGlnValAlaThrAlaLeuPro-----LeuGluLysProLeuAsnLeuVal 234
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